

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Levy, Gary
- (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: BERESKIN & PARR
 - (B) STREET: 40 King Street West
 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5H 3Y3
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Gravelle, Micheline
 - (B) REGISTRATION NUMBER: 40,261
 - (C) REFERENCE/DOCKET NUMBER: 9579-006
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (416) 364-7311
 - (B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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| TAAAGAGTCT GCCAACATTT TGAGAATGTG AATAGGATTT GGCTAAAATT AAGGGGATAT | 120 |
| ACAGAAAAGT CATAGGAAAT CAGGTAAAG ACATAAATAT GAGATAGGCT ACAGAGTGTT | 180 |
| TTAAGTAATA CAATAAACA TTTAGATTTT TGCCCATGTC AGTCATTTTG AAATTATTTT | 240 |
| TAAAGCAAAA AAACCCTTTT TAAACAAGAA ATCTTATGAG ATGTCAATAT GCAAAACAAA | 300 |
| TTAAAAGGAG GTGGTTTCTC TAACTGAAGC TGTCCTCTT TCCTGCCTTC AGCCTCTGAA | 360 |

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CAGGATCGAG GAGGTGTTCA AAGAAGTCCA AAACCTCAAG GAAATCGTAA ATAGTCTAAA 1620
GAAATCTTGC CAAGACTGCA AGCTGCAGGC TGATGACAAC GGAGACCCAG GCAGAAACGG 1680
ACTGTTGTTA CCCAGTACAG GAGCCCCGGG AGAGGTTGGT GATAACAGAG TTAGAGAATT 1740
AGAGAGTGAG GTTAACAAGC TGTCCTCTGA GCTAAAGAAT GCCAAAGAGG AGATCAATGT 1800
ACTTCATGGT CGCCTGGAGA AGCTGAATCT TGTAATATG AACAACATAG AAAATTATGT 1860
TGACAGCAAA GTGGCAAATC TAACATTTGT TGTCATAGT TTGGATGGCA AATGTTCAAA 1920
GTGTCCCAGC CAAGAACAAA TACAGTCACG TCCAGGTATG TATAATAATG TTTTCTTATC 1980
ATATGTTTCAT AAATGTTATA CAGTCAGAGA TGTATCTAAA AGATTAACCT GAGTCAGTAA 2040
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CTTCTCAAAT ATGACCACAT AAATATGACC TAATTACAAA ATCATAGTTA GTTCTGTATC 2160
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TACTTGGGAG GCTGAGGCAG GAGAATCGCT TGAACCTGAG AGGAAGAGGT TGCAGTGAGC 3720
CAAGAATGAG CCACTGCACT CCAGCATGGG TGACAGAGAA AACTCTGTCT CAAACAAAAA 3780
AATAATAAAA TTTATTCAGT AGGTGGATTC TACACAAAGT AATCTGTATT TGGGCCATGA 3840
TTTAAGCACA TCTGAAGGTA TATCACTCTT TTCAGGCTAT AATTATTTGG GTAATCTTCA 3900
TTCTGAGACA AACTTAATCT ATATCATTTA CTTTGCAACA GAACAACCCT ACAGCATTTT 3960
GGTTCCCAGA CTAAGGGAAC TAATATCTAT ATAATTAAAC TTGTTCATTT ATCATTCATG 4020
AAATATAAAA TACTTGTCAT TTAAACCGTT TAAAAATGTG GTAGCATAAT GTCACCCCAA 4080
AAAGCATTCA GAAAGCAATG TAACTGTGAA GACCAGGGTT TAAAGGTAAT TCATTTATAG 4140
TTTATAACTC CTTAGATGTT TGATGTTGAA AACTGCTTTA ACATGAAAAT TATCTTCCTC 4200
TGCTCTGTGT GAACAATAGC TTTTAATTTA AGATTGCTCA CTACTGTACT AGACTACTGG 4260
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CTATCATACT CTGAGGCCAA TTTTATCTCC AAAGCAATAA TATCATTAAG TGATTCACTT 4380
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 AGTAGTTAAA ATACTATATA TTTCAACCCT GGCTGGTAGA TTGCTTATTT TACTATCAGA 4500
 AACTAAAAGA TAGATTTTTA CCCAAACAGA AGTATCTGTA ATTTTATAA TTCATCAATT 4560
 CTGGAATGCT ATATATAATA TTAAAAGAC TTTTAAATG TGTTTAATTT CATCATCGTA 4620
 AAAAGGGATC 4630

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Ala Asn Trp Tyr Trp Leu Ser Ser Ala Val Leu Ala Thr
 1 5 10 15
 Tyr Gly Phe Leu Val Val Ala Asn Asn Glu Thr Glu Glu Ile Lys Asp
 20 25 30
 Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys
 35 40 45
 Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu
 50 55 60
 Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys
 65 70 75 80
 Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Lys Ser Cys
 85 90 95
 Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn
 100 105 110
 Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn
 115 120 125
 Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu
 130 135 140
 Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys
 145 150 155 160
 Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys
 165 170 175
 Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser
 180 185 190
 Lys Cys Pro Ser Gln Glu Gln Ile Gln Ser Arg Pro Val Gln His Leu
 195 200 205
 Ile Tyr Lys Asp Cys Ser Asp Tyr Tyr Ala Ile Gly Lys Arg Ser Ser
 210 215 220

439 amino acids

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Glu Thr Tyr Arg Val Thr Pro Asp Pro Lys Asn Ser Ser Phe Glu Val
 225 230 235 240
 Tyr Cys Asp Met Glu Thr Met Gly Gly Gly Trp Thr Val Leu Gln Ala
 245 250 255
 Arg Leu Asp Gly Ser Thr Asn Phe Thr Arg Thr Trp Gln Asp Tyr Lys
 260 265 270
 Ala Gly Phe Gly Asn Leu Arg Arg Glu Phe Trp Leu Gly Asn Asp Lys
 275 280 285
 Ile His Leu Leu Thr Lys Ser Lys Glu Met Ile Leu Arg Ile Asp Leu
 290 295 300
 Glu Asp Phe Asn Gly Val Glu Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr
 305 310 315 320
 Val Ala Asn Glu Phe Leu Lys Tyr Arg Leu His Val Gly Asn Tyr Asn
 325 330 335
 Gly Thr Ala Gly Asp Ala Leu Arg Phe Asn Lys His Tyr Asn His Asp
 340 345 350
 Leu Lys Phe Phe Thr Thr Pro Asp Lys Asp Asn Asp Arg Tyr Pro Ser
 355 360 365
 Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly Trp Trp Phe Asp Ala Cys
 370 375 380
 Leu Ser Ala Asn Leu Asn Gly Lys Tyr Tyr His Gln Lys Tyr Arg Gly
 385 390 395 400
 Val Arg Asn Gly Ile Phe Trp Gly Thr Trp Pro Gly Val Ser Glu Ala
 405 410 415
 His Pro Gly Gly Tyr Lys Ser Ser Phe Lys Glu Ala Lys Met Met Ile
 420 425 430
 Arg Pro Lys His Phe Lys Pro
 435

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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 TGAAGGCTCA GCAAAGCCAA TACGTGTTAT GTCCAGTTGG AGACAGTGCC AGGGCCAACA 180
 TTCCAGACTT CTCAGATAGA AAGTGCGCCT GCCTGCCCTG CTCTGAGAAT TTGAAGAGAG 240
 TAGTTCAGTT AGAATTAAGA GGCAGTAGAG AAAAGTCTTG GGAAATCTGG TTAGAGATAT 300
 AAATATGAGA ACTGGACATG GTGGTACACA CCTGTGATCT CTGTGTTTAG GAGGGAGAGG 360

CAGAGAGATC AGGAGTTCAA GGCCAGCCTG AGCTACTTGA GACCCAGTCT AAATAAATAA 420
 GAGATAGATT ACAGAGTGCC TTAACTAGT ACAGAGAAAG AATTTGGGTT TATCTGTGTC 480
 AGTTACGCTG AAATAATTTT TAAGTAATAA AATCCCTTTT AATAAGAAAC CTTATGAGGT 540
 CAGTATGCAC AATGAACTTA AGAGAGACCC CCAGCTCCTG AGCTGAGTGA TGGGGAAGGA 600
 CAGCCACTGC CTGTGATGTG TGAGTGACGT GCTTCCAAGT GTTTTAACCA CTGACGATTA 660
 CATAGCCTGC ACAGTCAGGA GAAAACAGCC GTATTCTCTG CCAGTTCTCT TCCCTTTTAC 720
 AAACAGATGA GAGACACACA CAGAGAATCC ATTTAAAGAG CGGACCTTTG TTCTGATTAG 780
 GGGCAATTTT AAGTACTTAA GAGTTCACAC AAAGTCTAGC CTTCAAAAAG AAAACAGGTT 840
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 TGCATAGTTT TGA CTGACAG GAGATGACAG CATTTGGCTG GCTGCGCTTG CTGAGGACCC 1140
 TCTCCTCCTG TGTGGCGTCT GAGACTGTGA TGCAAATGCG CCCGCCCTTT TCTGGGAACT 1200
 CAGAACGCCT GAGTCAGGCG GCGGTGGCTA TTAAAGCGCC TGGTCAGGCT GGGCTGCCGC 1260
 ACTGCAAGGA TGAGGCTTCC TGGTTGGTTG TGGCTGAGTT CTGCCGTCCT CGCTGCCTGC 1320
 CGAGCGGTGG AGGAGCACAA CCTGACTGAG GGGCTGGAGG ATGCCAGCGC CCAGGCTGCC 1380
 TGCCCCGCGA GGCTGGAGGG CAGCGGGAGG TGCGAGGGGA GCCAGTGCCC CTTCCAGCTC 1440
 ACCCTGCCCA CGCTGACCAT CCAGCTCCCG CGGCAGCTTG GCAGCATGGA GGAGGTGCTC 1500
 AAAGAAGTGC GGACCCTCAA GGAAGCAGTG GACAGTCTGA AGAAATCCTG CCAGGACTGT 1560
 AAGTTGCAGG CTGACGACCA TCGAGATCCC GGC GGGAATG GAGGGAATGG AGCAGAGACA 1620
 GCCGAGGACA GTAGAGTCCA GGA ACTGGAG AGTCAGGTGA ACAAGCTGTC CTCAGAGCTG 1680
 AAGAATGCAA AGGACCAGAT CCAGGGGCTG CAGGGGCGCC TGGAGACGCT CCATCTGGTA 1740
 AATATGAACA ACATTGAGAA CTACGTGGAC AACAAAGTGG CAAATCTAAC CGTTGTGGTC 1800
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- 70 -

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 TCAACGTTCT AGGAAGCTGA CTTTCTAGA ACAAATGTAT TTATTAGGAT GAATTTGGGA 5400
 ATT 5403

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Cys	Arg	Ala	Val	Glu	Glu	His	Asn	Leu	Thr	Glu	Gly	Leu	Glu	Asp	Ala
			20					25					30		
Ser	Ala	Gln	Ala	Ala	Cys	Pro	Ala	Arg	Leu	Glu	Gly	Ser	Gly	Arg	Cys
			35				40					45			
Glu	Gly	Ser	Gln	Cys	Pro	Phe	Gln	Leu	Thr	Leu	Pro	Thr	Leu	Thr	Ile
	50					55				60					
Gln	Leu	Pro	Arg	Gln	Leu	Gly	Ser	Met	Glu	Glu	Val	Leu	Lys	Glu	Val
55				70					75					80	

- 71 -

Arg Thr Leu Lys Glu Ala Val Asp Ser Leu Lys Lys Ser Cys Gln. Asp
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 Cys Lys Leu Gln Ala Asp Asp His Arg Asp Pro Gly Gly Asn Gly Gly
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 Gln Val Asn Lys Leu Ser Ser Glu Leu Lys Asn Ala Lys Asp Gln Ile
 130 135 140
 Gln Gly Leu Gln Gly Arg Leu Glu Thr Leu His Leu Val Asn Met Asn
 145 150 155 160
 Asn Ile Glu Asn Tyr Val Asp Asn Lys Val Ala Asn Leu Thr Val Val
 165 170 175
 Val Asn Ser Leu Asp Gly Lys Cys Ser Lys Cys Pro Ser Gln Glu His
 180 185 190
 Met Gln Ser Gln Pro Val Gln His Leu Ile Tyr Lys Asp Cys Ser Asp
 195 200 205
 His Tyr Val Leu Gly Arg Arg Ser Ser Gly Ala Tyr Arg Val Thr Pro
 210 215 220
 Asp His Arg Asn Ser Ser Phe Glu Val Tyr Cys Asp Met Glu Thr Met
 225 230 235 240
 Gly Gly Gly Trp Thr Val Leu Gln Ala Arg Leu Asp Gly Ser Thr Asn
 245 250 255
 Phe Thr Arg Glu Trp Lys Asp Tyr Lys Ala Gly Phe Gly Asn Leu Glu
 260 265 270
 Arg Glu Phe Trp Leu Gly Asn Asp Lys Ile His Leu Leu Thr Lys Ser
 275 280 285
 Lys Glu Met Ile Leu Arg Ile Asp Leu Glu Asp Phe Asn Gly Leu Thr
 290 295 300
 Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr Val Ala Asn Glu Phe Leu Lys
 305 310 315 320
 Tyr Arg Leu His Ile Gly Asn Tyr Asn Gly Thr Ala Gly Asp Ala Leu
 325 330 335
 Arg Phe Ser Arg His Tyr Asn His Asp Leu Arg Phe Phe Thr Thr Pro
 340 345 350
 Asp Arg Asp Asn Asp Arg Tyr Pro Ser Gly Asn Cys Gly Leu Tyr Tyr
 355 360 365
 Ser Ser Gly Trp Trp Phe Asp Ser Cys Leu Ser Ala Asn Leu Asn Gly
 370 375 380
 Lys Tyr Tyr His Gln Lys Tyr Lys Gly Val Arg Asn Gly Ile Phe Trp
 385 390 395 400
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 Ser Phe Lys Gln Ala Lys Met Met Ile Arg Pro Lys Asn Phe Lys Pro
 420 425 430

SEQUENCE LISTING



<110> Levy, Gary

<120> Methods of Modulating Immune Coagulation

<130> 9579-37

<140>

<141>

<150> US 09/442,143

<151> 1999-11-15

<160> 53

<170> PatentIn version 3.1

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21

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